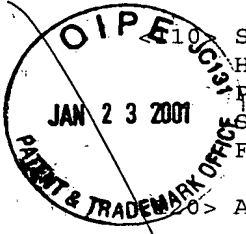


SEQUENCE LISTING

attachment # 7



<10> Sukhapinda, Kitisri
 Hasler, James M
 Petell, James K
 Strickland, James A
 Folkerts, Otto

<20> ANTIBODY-MEDIATED DOWN-REGULATION OF PLANT PROTEINS

<130> 50447

<140> US 09/358,321

<141> 1999-07-21

<150> US 60/093,587

<151> 1998-07-21

<160> 56

<170> PatentIn Ver. 2.0

<210> 1

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<220>

<221> unsure

<222> (12)

<223> n can be a,t,g, or c in this degenerate primer

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gargaraaym gncaygg

17

<210> 2

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<220>

<221> unsure

<222> (7)

<223> n can be a,t,g, or c in this degenerate primer

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18

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<211> 276

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<213> Zea mays

<220>
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 1 5 10 15
 ggg agg gtg gat atg agg cag att gag aag aca att cag tat ctt att 96
 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
 20 25 30
 ggc tct gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc 144
 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
 35 40 45
 atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac ggg aac 192
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
 50 55 60
 act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca caa atc 240
 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
 65 70 75 80
 tgc ggc atc atc gcc tca gat gag aag cga cat gaa 276
 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
 85 90

<210> 4
 <211> 92
 <212> PRT
 <213> Zea mays

<400> 4
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 1 5 10 15
 Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
 20 25 30
 Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe
 35 40 45
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
 50 55 60
 Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile
 65 70 75 80
 Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu
 85 90

<210> 5
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 <212> DNA
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<220>
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<222> (146)..(1324)

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<400> 5
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atcccaatct cgcgaggggca agcagcaggg tctgcggcgg cggcggcggc cgcgcttccg 120

gctcccccttc ccattggcct ccacg atg gcg ctc cgc ctc aac gac gtc gcg 172
Met Ala Leu Arg Leu Asn Asp Val Ala
-30 -25

ctc tgc ctc tcc ccg ccg ctc gcc gcc cgc cgc cgc cgc cgc agc agc 220
Leu Cys Leu Ser Pro Pro Leu Ala Ala Arg Arg Arg Arg Arg Ser Ser
-20 -15 -10

ggc agg ttc gtc gcc gtc gcc tcc atg acg tcc gcc gtc tcc acc aag 268
Gly Arg Phe Val Ala Val Ala Ser Met Thr Ser Ala Val Ser Thr Lys
-5 -1 1 5 10

gtc gag aat aag aag cca ttt gct cct cca agg gag gta cat gtc cag 316
Val Glu Asn Lys Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln
15 20 25

gtt aca cat tca atg cca cct cac aag att gaa att ttc aag tcg ctt 364
Val Thr His Ser Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu
30 35 40

gat gat tgg gct aga gat aat atc ttg acg cat ctc aag cca gtc gag 412
Asp Asp Trp Ala Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu
45 50 55

aag tgt tgg cag cca cag gat ttc ctc ccg gac cca gca tct gaa gga 460
Lys Cys Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly
60 65 70

ttt cat gat gaa gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct 508
Phe His Asp Glu Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro
75 80 85 90

gat gat tat ttt gtt tgt ttg gtg gga gac atg att acc gag gaa gct 556
Asp Asp Tyr Phe Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala
95 100 105

cta cca aca tac cag act atg ctt aac acc ctc gac ggt gtc aga gat 604
Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp
110 115 120

gag aca ggt gca agc ccc act gcc tgg gct gtt tgg acg agg gca tgg 652
Glu Thr Gly Ala Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp
125 130 135

act gct gag gag aac agg cat ggt gat ctg ctc aac aag tat atg tac 700
Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr
140 145 150

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ctc act ggg agg gtg gat atg agg cag att gag aag aca att cag tat	748
Leu Thr Gly Arg Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr	
155 160 165 170	
ctt att ggc tct gga atg gat cct agg act gag aat aat cct tat ctt	796
Leu Ile Gly Ser Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu	
175 180 185	
ggg ttc atc tac acc tcc ttc caa gag cgg gcg acc ttc atc tca cac	844
Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His	
190 195 200	
ggg aac act gct cgt cac gcc aag gac ttt ggc gac tta aag ctt gca	892
Gly Asn Thr Ala Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala	
205 210 215	
caa atc tgc ggc atc atc gcc tca gat gag aag cga cat gaa act gcg	940
Gln Ile Cys Gly Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala	
220 225 230	
tac acc aag atc gtg gag aag ctg ttt gag atc gac cct gat ggt acc	988
Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr	
235 240 245 250	
gtg gtc gct ctg gct gac atg atg agg aag aag atc tca atg cct gcc	1036
Val Val Ala Leu Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala	
255 260 265	
cac ctg atg ttt gac ggg cag gac gac aag ctg ttc gag cac ttc tcc	1084
His Leu Met Phe Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser	
270 275 280	
atg gtc gcg cag agg ctt ggc gtt tac acc gcc agg gac tac gcc gac	1132
Met Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp	
285 290 295	
atc ctc gag ttc ctc gtc gac agg tgg aag gtg gcg agc ctg act ggt	1180
Ile Leu Glu Phe Leu Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly	
300 305 310	
ctg tcg ggt gaa ggg aac aag gcg cag gac tac ctt tgc acc ctt gct	1228
Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala	
315 320 325 330	
tca aga atc agg agg ctg gag gag agg gcc cag agc aga gcc aag aaa	1276
Ser Arg Ile Arg Arg Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys	
335 340 345	
gcc ggc acg ctg cct ttc agc tgg gta tac ggt agg gac gtc caa ctg	1324
Ala Gly Thr Leu Pro Phe Ser Trp Val Tyr Gly Arg Asp Val Gln Leu	
350 355 360	
tgagatcgga aacctgctgc ggactgctta gacaagacct gctgtgtctg cgttacatag	1384
gtctccaggt tttgatcaaa tgggtcccggtg tcgtcttata gagcgatagg agaacgtggt	1444
gggtctgtggt gtagctttgt ttttattttg tattttttctg ctttgatgta caacctgtgg	1504
ccgcatgaac tggggcgtgg agatgggagc gaccatgccg tactttgtct gtcgctggcg	1564
gtgtgtttcg gtatgttatt tgagttgtc agatctgtta aaaaaaaaaa aaaaaaa	1621

<210> 6
 <211> 393
 <212> PRT
 <213> Zea mays

<400> 6
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 -15 -10 -5 -1 1
 Ser Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys Pro Phe
 5 10 15
 Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met Pro Pro
 20 25 30
 His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asp Asn
 35 40 45
 Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp
 50 55 60 65
 Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val Lys Glu
 70 75 80
 Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Cys Leu
 85 90 95
 Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met
 100 105 110
 Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr
 115 120 125
 Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His
 130 135 140 145
 Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val Asp Met
 150 155 160
 Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp
 165 170 175
 Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe
 180 185 190
 Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg His Ala
 195 200 205
 Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile Ile Ala
 210 215 220 225
 Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys
 230 235 240
 Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala Asp Met
 245 250 255

Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln
260 265 270

Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly
275 280 285

Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp
290 295 300 305

Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys
310 315 320

Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Glu
325 330 335

Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser
340 345 350

Trp Val Tyr Gly Arg Asp Val Gln Leu
355 360

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
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<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 8
aaagctagct catcacagtt ggacgtccct accgta 36

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
accatggcta gcatgacgtc cgccgtctcc 30

<210> 10
<211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 10
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<210> 11
 <211> 1107
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (4)..(1092)

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 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys
 1 5 10 15

aag cca ttt gct cct cca agg gag gta cat gtc cag gtt aca cat tca 96
 Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser
 20 25 30

atg cca cct cac aag att gaa att ttc aag tcg ctt gat gat tgg gct 144
 Met Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala
 35 40 45

aga gat aat atc ttg acg cat ctc aag cca gtc gag aag tgt tgg cag 192
 Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln
 50 55 60

cca cag gat ttc ctc ccg gac cca gca tct gaa gga ttt cat gat gaa 240
 Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu
 65 70 75

gtt aag gag ctc aga gaa cgt gcc aag gaa atc cct gat gat tat ttt 288
 Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
 80 85 90 95

gtt tgt ttg gtg gga gac atg att acc gag gaa gct cta cca aca tac 336
 Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
 100 105 110

cag act atg ctt aac acc ctc gac ggt gtc aga gat gag aca ggt gca 384
 Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
 115 120 125

agc ccc act gcc tgg gct gtt tgg acg agg gca tgg act gct gag gag 432
 Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu
 130 135 140

aac agg cat ggt gat ctg ctc aac aag tat atg tac ctc act ggg agg 480
 Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg
 145 150 155

gtg gat atg agg cag att gag aag aca att cag tat ctt att ggc tct 528

Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	
160					165					170					175	
gga	atg	gat	cct	agg	act	gag	aat	aat	cct	tat	ctt	ggt	ttc	atc	tac	576
Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr	
				180					185					190		
acc	tcc	ttc	caa	gag	cgg	gcg	acc	ttc	atc	tca	cac	ggg	aac	act	gct	624
Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	
			195					200					205			
cgt	cac	gcc	aag	gac	ttt	ggc	gac	tta	aag	ctt	gca	caa	atc	tgc	ggc	672
Arg	His	Ala	Lys	Asp	Phe	Gly	Asp	Leu	Lys	Leu	Ala	Gln	Ile	Cys	Gly	
		210					215					220				
atc	atc	gcc	tca	gat	gag	aag	cga	cat	gaa	act	gcg	tac	acc	aag	atc	720
Ile	Ile	Ala	Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	
		225				230					235					
gtg	gag	aag	ctg	ttt	gag	atc	gac	cct	gat	ggg	acc	gtg	gtc	gct	ctg	768
Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Val	Ala	Leu	
240					245					250				255		
gct	gac	atg	atg	agg	aag	aag	atc	tca	atg	cct	gcc	cac	ctg	atg	ttt	816
Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro	Ala	His	Leu	Met	Phe	
				260					265					270		
gac	ggg	cag	gac	gac	aag	ctg	ttc	gag	cac	ttc	tcc	atg	gtc	gcg	cag	864
Asp	Gly	Gln	Asp	Asp	Lys	Leu	Phe	Glu	His	Phe	Ser	Met	Val	Ala	Gln	
			275					280					285			
agg	ctt	ggc	gtt	tac	acc	gcc	agg	gac	tac	gcc	gac	atc	ctc	gag	ttc	912
Arg	Leu	Gly	Val	Tyr	Thr	Ala	Arg	Asp	Tyr	Ala	Asp	Ile	Leu	Glu	Phe	
		290					295					300				
ctc	gtc	gac	agg	tgg	aag	gtg	gcg	agc	ctg	act	ggg	ctg	tcg	ggg	gaa	960
Leu	Val	Asp	Arg	Trp	Lys	Val	Ala	Ser	Leu	Thr	Gly	Leu	Ser	Gly	Glu	
		305				310					315					
ggg	aac	aag	gcg	cag	gac	tac	ctt	tgc	acc	ctt	gct	tca	aga	atc	agg	1008
Gly	Asn	Lys	Ala	Gln	Asp	Tyr	Leu	Cys	Thr	Leu	Ala	Ser	Arg	Ile	Arg	
320					325					330					335	
agg	ctg	gag	gag	agg	gcc	cag	agc	aga	gcc	aag	aaa	gcc	ggc	acg	ctg	1056
Arg	Leu	Glu	Glu	Arg	Ala	Gln	Ser	Arg	Ala	Lys	Lys	Ala	Gly	Thr	Leu	
				340					345					350		
cct	ttc	agc	tgg	gta	tac	ggg	agg	gac	gtc	caa	ctg	tgagctagca	tcac			1107
Pro	Phe	Ser	Trp	Val	Tyr	Gly	Arg	Asp	Val	Gln	Leu					
			355					360								

<210> 12
 <211> 363
 <212> PRT
 <213> Zea mays

<400> 12
 Met Ala Thr Met Thr Ser Ala Val Ser Thr Lys Val Glu Asn Lys Lys
 1 5 10 15

Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met
 20 25 30
 Pro Pro His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg
 35 40 45
 Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro
 50 55 60
 Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val
 65 70 75 80
 Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val
 85 90 95
 Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln
 100 105 110
 Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser
 115 120 125
 Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn
 130 135 140
 Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val
 145 150 155 160
 Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly
 165 170 175
 Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr
 180 185 190
 Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg
 195 200 205
 His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile
 210 215 220
 Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val
 225 230 235 240
 Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala
 245 250 255
 Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp
 260 265 270
 Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg
 275 280 285
 Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu
 290 295 300
 Val Asp Arg Trp Lys Val Ala Ser Leu Thr Gly Leu Ser Gly Glu Gly
 305 310 315 320
 Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg
 325 330 335
 Leu Glu Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro

<220>
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 <400> 17
 aaagctagcc tsctgcygyt ctkkttwycw ggtryc 36

 <210> 18
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 18
 tacgttacct gageggccgc gctgggctca agttttttgt ccaccg 46

 <210> 19
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 19
 ttgctagct tactaacact cattcctggt gaagctct 38

 <210> 20
 <211> 102
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 20
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 cattctgcct ttgcggcggt tgtgatgacc ccaaaccac tc 102

 <210> 21
 <211> 738
 <212> DNA
 <213> mouse

 <220>
 <221> unsure
 <222> (16) .. (21)
 <223> not known

 <220>
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 <222> (26)
 <223> not known

 <220>

<221> unsure
 <222> (32)
 <223> not known

<220>
 <221> CDS
 <222> (37) .. (693)

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				Asp	Val	Val	Met	Thr	Pro	
				1				5		
aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	102									
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser										
	10	15	20							
tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta	150									
Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu										
	25	30	35							
cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac	198									
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr										
	40	45	50							
aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt	246									
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser										
	55	60	65	70						
gga tca ggg aca gat ttc aca ctc aag atc aac aga gtg gag gct gag	294									
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Asn Arg Val Glu Ala Glu										
	75	80	85							
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg	342									
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr										
	90	95	100							
ttc gga ggg ggg acc aag ctg gaa ata aaa cgg gct gat gct gca cca	390									
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro										
	105	110	115							
act gta tcc atc ttc cca cca tcc agt gag cag tta aca tct gga ggt	438									
Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly										
	120	125	130							
gcc tca gtc gtg tgc ttc ttg aac aac ttc tac ccc aaa gac atc aat	486									
Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn										
	135	140	145	150						
gtc aag tgg aag att gat ggc agt gaa cga caa aat ggc gtc ctg aac	534									
Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn										
	155	160	165							
agt tgg act gat cag gac acc aaa gac agc acc tac agc atg agc agc	582									
Ser Trp Thr Asp Gln Asp Thr Lys Asp Ser Thr Tyr Ser Met Ser Ser										
	170	175	180							
acc ctc acg ttg acc aag gac gag tat gaa cga cat aac agc tat acc	630									
Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr										
	185	190	195							

tgt gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc	678
Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe	
200 205 210	

aac agg aat gag tgt tagtaagcta gcacgcccga tgggtgggacg gtatgaataa	733
Asn Arg Asn Glu Cys	
215	

tccgg	738
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<210> 22
 <211> 336
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(336)

<400> 22	
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Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly	
1 5 10 15	

gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	

aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	

cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	

gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

aac aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt	288
Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser	
85 90 95	

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa	336
Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
100 105 110	

<210> 23
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 <212> DNA
 <213> Artificial Sequence

<220>
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108

<210> 24
<211> 882
<212> DNA
<213> mouse

<220>
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<222> (25)..(837)

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<222> (79)..(837)

<400> 24
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-15 -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
-5 -1 1 5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
10 15 20

aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat 195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His
25 30 35

tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa 243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
40 45 50 55

gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
60 65 70

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat 339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
75 80 85

ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc 387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe
90 95 100

gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc 435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly
105 110 115

aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag 483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln
120 125 130 135

cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc 531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser
140 145 150

tgc aag gct tgc ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
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His His His His His His	
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1 5 10 15	
gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
20 25 30	
aat gga atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct	144
Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	
cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	
gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	

agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95

aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
 Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

ggc 339
 Gly

<210> 26
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 26
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 agtc 64

<210> 27
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 27
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 aac 63

<210> 28
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 28
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<210> 29
 <211> 459
 <212> DNA
 <213> mouse

<220>

<221> CDS
 <222> (19)..(459)

<220>
 <221> mat_peptide
 <222> (79)..(459)

<400> 29
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 Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu
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gcg gcg gcg gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct 99
 Ala Ala Ala Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser
 -5 -1 1 5

ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag 147
 Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys
 10 15 20

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg cag 195
 Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln
 25 30 35

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act 243
 Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr
 40 45 50 55

ggg ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act 291
 Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr
 60 65 70

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca 339
 Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr
 75 80 85

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg 387
 Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp
 90 95 100

ggc caa ggg act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga 435
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly
 105 110 115

tct ggc tcc gaa tcc aaa ccc ggg 459
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<210> 30
 <211> 438
 <212> DNA
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<220>
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 <222> (1)..(408)

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gtg atg acc cca aac cca ctc tcc ctg cct gtc agt ctt gga gat caa	96			
Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln				
20 25 30				
gcc tcc atc tct tgc aga tct agt cag agc ctt tta cac agt aat gga	144			
Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly				
35 40 45				
atc acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aag	192			
Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys				
50 55 60				
ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg	240			
Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg				
65 70 75 80				
ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga	288			
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg				
85 90 95				
gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat	336			
Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His				
100 105 110				
gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gaa gaa	384			
Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu Glu				
115 120 125				
aaa ctc atc tca gaa gag gat ctg aattagtaag gggccgcctt gacctagtgc	438			
Lys Leu Ile Ser Glu Glu Asp Leu				
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<400> 31				
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gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96			
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu				
-5 -1 1 5 10				
ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tcg ggc	144			
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly				
15 20 25				

tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gag ggt aaa tcc tca gga tct ggc tcc	432
Thr Leu Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser	
110 115 120	
gaa tcc aaa ccc ggg gat gtt gtg atg acc cca aac cca ctc tcc ctg	480
Glu Ser Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu	
125 130 135	
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag	528
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln	
140 145 150	
agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac ctg cag	576
Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln	
155 160 165 170	
aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga	624
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg	
175 180 185	
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat	672
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
190 195 200	
ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat	720
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr	
205 210 215	
ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc	768
Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr	
220 225 230	
aag ctg gaa ata aaa gaa gaa aaa ctc atc tca gaa gag gat ctg	813
Lys Leu Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu	
235 240 245	
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<210> 32

<211> 269

<212> PRT
 <213> mouse

<400> 32

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          -1    1          5          10

Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr
          15          20          25

Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val His Gly
          30          35          40

Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr
          45          50          55          60

Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser
          65          70          75

Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala
          80          85          90

Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu
          95          100          105

Val Thr Val Ser Ala Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser
          110          115          120

Lys Pro Gly Asp Val Val Met Thr Pro Asn Pro Leu Ser Leu Pro Val
125          130          135          140

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
          145          150          155

Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
          160          165          170

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
          175          180          185

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
          190          195          200

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
205          210          215          220

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
          225          230          235

Glu Ile Lys Glu Glu Lys Leu Ile Ser Glu Glu Asp Leu
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<210> 33
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:c-myc tag

<400> 33
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<210> 34
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:p67 leader

<400> 34
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<210> 35
 <211> 84
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 35
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 gccgtcaacg ctgcggttgt gatg 84

<210> 36
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 36
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<210> 37
 <211> 74
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 37
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 caactgcagc agtc 74

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<210> 38
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 38
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gtgaccagag tc 72

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<210> 39
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 39
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<210> 40
<211> 462
<212> DNA
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<220>
<221> CDS
<222> (19)..(462)

<220>
<221> mat_peptide
<222> (73)..(462)

<400> 40
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act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca aac cca ctc 99
Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu
-5 -1 1 5

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct 147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
10 15 20 25

agt cag agc ctt tta cac agt aat gga atc acc tat tta cat tgg tac 195
Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr
30 35 40

ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc 243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
45 50 55

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg 291

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Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly		
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Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly		
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Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly		
	90				95				100					105			
ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	ggc	aag	ccg	435	
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro		
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ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc								462	
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Lys	Gly	His	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro		
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Gly	Ala	Ser	Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr		
		35					40					45					
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Trp	Ile	Gly	Ala	Ile	Asp	Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln		
	65				70				75					80			
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Lys	Phe	Lys	Asp	Lys	Ala	Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr		
			85						90					95			
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Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr		
			100					105					110				
tac	tat	aca	aga	tgg	ttt	gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	384	
Tyr	Tyr	Thr	Arg	Trp	Phe	Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr		
		115					120					125					

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<210> 42
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 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (19)..(831)

<220>
 <221> mat_peptide
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Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro Asn Pro Leu	
-5 -1 1 5	
tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct	147
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser	
10 15 20 25	
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Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp Tyr	
30 35 40	
ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc	243
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser	
45 50 55	
aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg	291
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly	
60 65 70	
aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga	339
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly	
75 80 85	
gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg	387
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly	
90 95 100 105	
ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag ccg	435
Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro	
110 115 120	
ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag tct	483
Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln Ser	
125 130 135	


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ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag 531
Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys
      140                      145                      150

gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg aag cag 579
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Lys Gln
      155                      160                      165

aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa act 627
Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr
      170                      175                      180                      185

ggg ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg act 675
Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr
      190                      195                      200

gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca 723
Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr
      205                      210                      215

tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg 771
Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp
      220                      225                      230

ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat cat 819
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His His
      235                      240                      245

cat cat cat cat gcggccgctt gacctagtgc 851
His His His His
250

<210> 43
<211> 867
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (31)..(843)

<220>
<221> mat_peptide
<222> (85)..(843)

<400> 43
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Met Thr Ile Leu Cys Trp Leu Ala
      -15

ctt ctg tca act ctg act gcc gtc aac gct gcg gtt gtg atg acc cca 102
Leu Leu Ser Thr Leu Thr Ala Val Asn Ala Ala Val Val Met Thr Pro
-10                      -5                      -1      1                      5

aac cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 150
Asn Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
      10                      15                      20

tgc aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta 198

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Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu		
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cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	246	
His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr		
	40					45					50						
aaa	ggt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	294	
Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
	55				60					65					70		
gga	tca	ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	342	
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu		
				75					80					85			
gat	ctg	gga	ggt	tat	ttc	tgc	tct	caa	agt	aca	cat	ggt	ccg	tac	acg	390	
Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr		
			90					95					100				
ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa	ggc	agc	acc	agc	ggc	agc	438	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser		
		105					110					115					
ggc	aag	ccg	ggc	agc	ggc	gag	ggc	agc	acc	aag	ggc	cat	ggt	caa	ctg	486	
Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	His	Val	Gln	Leu		
	120					125					130						
cag	cag	tct	ggg	gct	gag	ctg	gtg	agg	cct	ggg	gct	tca	gtg	acg	ctg	534	
Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	Ser	Val	Thr	Leu		
	135				140					145					150		
tcc	tgc	aag	gct	tcg	ggc	tac	aca	ttt	act	gac	tat	gaa	ata	cac	tgg	582	
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Glu	Ile	His	Trp		
				155					160					165			
gtg	aag	cag	aca	cct	gtg	cat	ggc	ctg	gaa	tgg	att	gga	gct	att	gat	630	
Val	Lys	Gln	Thr	Pro	Val	His	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Asp		
			170					175					180				
cct	gaa	act	ggt	ggt	act	gcc	tac	aat	cag	aag	ttc	aag	gac	aag	gcc	678	
Pro	Glu	Thr	Gly	Gly	Thr	Ala	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala		
		185					190					195					
ata	gtg	act	gta	gac	aaa	tcc	tcc	agc	aca	gcc	tac	atg	gag	ctc	cgc	726	
Ile	Val	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg		
	200					205					210						
agc	ctg	aca	tct	gaa	gac	tct	gcc	gtc	tat	tac	tat	aca	aga	tgg	ttt	774	
Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Tyr	Thr	Arg	Trp	Phe		
	215				220					225					230		
gag	gac	tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	atg	cgg	ggt	822	
Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Met	Arg	Gly		
				235				240						245			
tct	cat	cat	cat	cat	cat	cat	cat	taggcggccg	ctgcagatct	gatac						867	
Ser	His	His	His	His	His	His											
			250														

<210> 44

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<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<210> 45
<211> 43
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<220>
<223> Description of Artificial Sequence:primer

<400> 45
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<210> 46
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<210> 47
<211> 882
<212> DNA
<213> mouse

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<222> (25)..(837)

<220>
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<222> (79)..(837)

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ctgcagggta cggccatatt ggcc atg act atc ctt tgc tgg ctg gcc ctt 51
                               Met Thr Ile Leu Cys Trp Leu Ala Leu
                               -15                               -10

ctg tca act ctg act gcc gtc aac act gcg gtt gtg atg acc cca aac 99
Leu Ser Thr Leu Thr Ala Val Asn Thr Ala Val Val Met Thr Pro Asn
      -5              -1   1              5

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 147
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
      10              15              20

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aga tct agt cag agc ctt tta cac agt aat gga atc acc tat tta cat	195
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His	
25 30 35	
tggtacctgcag aagcca ggc cag tctcca aagctcctg atctacaaa	243
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys	
40 45 50 55	
gtttccaac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga	291
Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly	
60 65 70	
tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat	339
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp	
75 80 85	
ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc	387
Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe	
90 95 100	
gga ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc	435
Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly	
105 110 115	
aag ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag	483
Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln	
120 125 130 135	
cag tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc	531
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser	
140 145 150	
tgc aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg	579
Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val	
155 160 165	
agg cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct	627
Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro	
170 175 180	
gaa act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata	675
Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile	
185 190 195	
gtg act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc	723
Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser	
200 205 210 215	
ctg aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag	771
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu	
220 225 230	
gac tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct	819
Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser	
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cat cat cat cat cat cat tagggcctct ctggccgata ccccgaaattt	867
His His His His His His	
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<222> (25)..(786)
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1 5

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Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu His Trp
30 35 40

tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt 195
Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val

45 50 55

tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca 243
Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
60 65 70

ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg 291
Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
75 80 85

gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga 339
Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
90 95 100 105

ggg ggg acc aag ctg gaa ata aaa ggc agc acc agc ggc agc ggc aag 387
Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys
110 115 120

ccg ggc agc ggc gag ggc agc acc aag ggc cat gtt caa ctg cag cag 435
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly His Val Gln Leu Gln Gln
125 130 135

tct ggg gct gag ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc 483
Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys
140 145 150

aag gct tcg ggc tac aca ttt act gac tat gaa ata cac tgg gtg agg 531
Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg
155 160 165

cag aca cct gtg cat ggc ctg gaa tgg att gga gct att gat cct gaa 579
Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu
170 175 180 185

act ggt ggt act gcc tac aat cag aag ttc aag gac aag gcc ata gtg 627

Thr Gly Gly Thr	Ala Tyr Asn Gln Lys	Phe Lys Asp Lys Ala	Ile Val	
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act gta gac aaa tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg				675
Thr Val Asp Lys Ser Ser Ser Thr	Ala Tyr Met Glu Leu Arg Ser Leu			
	205	210	215	
aca tct gaa gac tct gcc gtc tat tac tat aca aga tgg ttt gag gac				723
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp				
	220	225	230	
tgg ggc caa ggg act ctg gtc act gtc tct gca atg cgg ggt tct cat				771
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Met Arg Gly Ser His				
	235	240	245	
cat cat cat cat cat tagggcctct ctggccgata ccccgaaattt ccccgatcgt				826
His His His His His				
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<210> 49				
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<221> CDS				
<222> (19)..(687)				
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	Leu Val Thr Val Val Asp Gly Ala Gln Ser Gln			
	1	5	10	
gtt caa ctg cag cag tct ggg gct gag ctg gtg agg cct ggg gct tca				99
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser				
	15	20	25	
gtg acg ctg tcc tgc aag gct tgc ggc tac aca ttt act gac tat gaa				147
Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Glu				
	30	35	40	
ata cac tgg gtg agg cag aca cct gtg cat ggc ctg gaa tgg att gga				195
Ile His Trp Val Arg Gln Thr Pro Val His Gly Leu Glu Trp Ile Gly				
	45	50	55	
gct att gat cct gaa act ggt ggt act gcc tac aat cag aag ttc aag				243
Ala Ile Asp Pro Glu Thr Gly Gly Thr Ala Tyr Asn Gln Lys Phe Lys				
	60	65	70	75
gac aag gcc ata gtg act gta gac aaa tcc tcc agc aca gcc tac atg				291
Asp Lys Ala Ile Val Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met				
	80	85	90	
gag ctc cgc agc ctg aca tct gaa gac tct gcc gtc tat tac tat aca				339
Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr Thr				
	95	100	105	

aga tgg ttt gag gac tgg ggc caa ggg act ctg gtc act gtc tct gca	387
Arg Trp Phe Glu Asp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala	
110 115 120	
gcc aaa aca aca ccc cca tca gtc tat cca ctg gcc cct ggg tgt gga	435
Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Cys Gly	
125 130 135	
gat aca act ggt tcc tct gtg act ctg gga tgc ctg gtc aag ggc tac	483
Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr	
140 145 150 155	
ttc cct gag tca gtg act gtg act tgg aac tct gga tcc ctg tcc agc	531
Phe Pro Glu Ser Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser	
160 165 170	
agt gtg cac acc ttc cca gct ctc ctg cag tct gga ctc tac act atg	579
Ser Val His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Met	
175 180 185	
agc agc tca gtg act gtc ccc tcc agc acc tgg cca agt cag acc gtc	627
Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val	
190 195 200	
acc tgc agc gtt gct cac cca gcc agc agc acc acg gtg gac aaa aaa	675
Thr Cys Ser Val Ala His Pro Ala Ser Ser Thr Thr Val Asp Lys Lys	
205 210 215	
ctt gag ccc agc gcggccgctg caggtcttga tcctttcctg ggacccggca	727
Leu Glu Pro Ser	
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agaaccaaaa a	738
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Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala	
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gcg cat tct gcc ttt gcg gcg gtt caa ctg cag cag tct ggg gct gag	96
Ala His Ser Ala Phe Ala Ala Val Gln Leu Gln Gln Ser Gly Ala Glu	
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ctg gtg agg cct ggg gct tca gtg acg ctg tcc tgc aag gct tgc ggc	144
Leu Val Arg Pro Gly Ala Ser Val Thr Leu Ser Cys Lys Ala Ser Gly	
15 20 25	
tac aca ttt act gac tat gaa ata cac tgg gtg agg cag aca cct gtg	192
Tyr Thr Phe Thr Asp Tyr Glu Ile His Trp Val Arg Gln Thr Pro Val	
30 35 40	
cat ggc ctg gaa tgg att gga gct att gat cct gaa act ggt ggt act	240
His Gly Leu Glu Trp Ile Gly Ala Ile Asp Pro Glu Thr Gly Gly Thr	
45 50 55	
gcc tac aat cag aag ttc aag gac aag gcc ata gtg act gta gac aaa	288
Ala Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Val Thr Val Asp Lys	
60 65 70	
tcc tcc agc aca gcc tac atg gag ctc cgc agc ctg aca tct gaa gac	336
Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp	
75 80 85 90	
tct gcc gtc tat tac tat aca aga tgg ttt gag gac tgg ggc caa ggg	384
Ser Ala Val Tyr Tyr Tyr Thr Arg Trp Phe Glu Asp Trp Gly Gln Gly	
95 100 105	
act ctg gtc act gtc tct gca gcc aaa aca aca ccc cca tca gtc tat	432
Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr	
110 115 120	
cca ctg gcc cct ggg tgt gga gat aca act ggt tcc tct gtg act ctg	480
Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu	
125 130 135	
gga tgc ctg gtc aag ggc tac ttc cct gag tca gtg act gtg act tgg	528
Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp	
140 145 150	
aac tct gga tcc ctg tcc agc agt gtg cac acc ttc cca gct ctc ctg	576
Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu	
155 160 165 170	
cag tct gga ctc tac act atg agc agc tca gtg act gtc ccc tcc agc	624
Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser	
175 180 185	
acc tgg acc tgc agc gtt gct cac cca gcc agc agc cca agt cag acc	672
Thr Trp Thr Cys Ser Val Ala His Pro Ala Ser Ser Pro Ser Gln Thr	
190 195 200	
gtc acc acg gtg gac aaa aaa ctt gag ccc agc tagtaatgag cggccgctgc	725
Val Thr Thr Val Asp Lys Lys Leu Glu Pro Ser	
205 210	
agatctgac ctttctggg acccgga	753

<210> 52

<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 2253 to 2271
of pDAB439

<400> 52
tgcattgtgtt ctcctttttt 19

<210> 53
<211> 44
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 4256 to 4308
of pDAB439

<400> 53
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<210> 54
<211> 63
<212> DNA
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<220>

<223> Description of Artificial Sequence:nt 4744 to 4807
of pDAB439

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ggg 63

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nt 5417 to 5436
of pDAB439

<400> 55
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<210> 56
<211> 24
<212> PRT
<213> Zea mays

<400> 56
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1 5 10 15

Pro Glu Ser Leu Asp Val Arg Gly
20

<210> 57
<211> 12
<212> DNA
<213> Zea mays

<400> 57
atggcgctccgc 12

<210> 58
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: putative N-terminus of the precursor protein

<400> 58
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<210> 59
<211> 12
<212> PRT
<213> Zea Mays

<400> 59
Met-Ala-Leu-Arg 4

<210> 60
<211> 12
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<213> Artificial Sequence

<220>
<223> Description of Artifical Sequence: putative N-terminus of the precursor protein

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